

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2005, 04:28:43 ; Search time 79 Seconds  
(without alignments)  
440.613 Million cell

updates/sec

Title: US-10-644-807-213  
Perfect score: 505  
Sequence: 1 MDRRRMALRPGSRRPTAFF.....RWKPVAPRRMKACPQVLEW 90

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

		%					Description
Result	Query	Match	Length	DB	ID		
No.	Score						
-----							
1	505	100.0	90	5	ADG79407		Adg79407
Human sec							
2	505	100.0	90	5	ADG79496		Adg79496
Human sec							
3	505	100.0	90	8	ADP07884		Adp07884
Human sec.							

4	499	98.8	90	8	ADP07857	Adp07857
Human sec						
5	499	98.8	90	8	ADP07885	Adp07885
Human sec						
6	85.5	16.9	141	4	ABG19603	Abg19603
Novel hum						
7	76.5	15.1	414	7	ABO79149	Abo79149
Pseudomon						
8	76	15.0	181	8	ADS34928	Ads34928
Human aut						
9	76	15.0	202	3	AAB53434	Aab53434
Human col						
10	76	15.0	335	7	ABO78267	Abo78267
Pseudomon						
11	75.5	15.0	211	8	ABO84533	Abo84533
Human can						
12	75.5	15.0	211	8	ABO84531	Abo84531
Human can						
13	75.5	15.0	211	8	ADQ39469	Adq39469
Human myo						
14	75.5	15.0	211	8	ADQ39468	Adq39468
Human myo						
15	75	14.9	279	7	ADM26734	Adm26734
Hyperther						
16	75	14.9	470	7	ABO79058	Abo79058
Pseudomon						
17	74.5	14.8	428	7	ABO75706	Abo75706
Pseudomon						
18	73	14.5	329	7	ABO71006	Abo71006
Pseudomon						
19	73	14.5	525	4	ABG16066	Abg16066
Novel hum						
20	72.5	14.4	109	4	AAO00711	Aao00711
Human pol						
21	72	14.3	88	4	AAU41359	Aau41359
Propionib						
22	72	14.3	88	6	ABM37878	Abm37878
Propionib						
23	71.5	14.2	168	3	AAAY68732	Aay68732
Amino aci						
24	71.5	14.2	179	3	AAAY68731	Aay68731
Amino aci						
25	71.5	14.2	203	8	ABM81474	Abm81474
Tumour-as						
26	71.5	14.2	578	7	ABO69910	Abo69910
Pseudomon						
27	71	14.1	104	4	AAO07492	Aao07492
Human pol						
28	70.5	14.0	340	7	ABO61408	Abo61408
Klebsiell						
29	70.5	14.0	520	6	ABP98903	Abp98903
Human mol						
30	70.5	14.0	568	7	ADI60254	Adi60254
Secreted						
31	70.5	14.0	603	8	ADG98231	Adg98231
Acyl-spec						

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OM protein - protein search, using sw model

Run on: October 26, 2005, 04:30:26 ; Search time 20 Seconds  
(without alignments)  
432.975 Million cell

updates/sec

Title: US-10-644-807-213  
Perfect score: 505  
Sequence: 1 MDRRRMALRPGSRRPTAFF.....RWKPVAPRRMKACPQVLLEW 90

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pirl:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being  
printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	70	13.9	995	2	T51051		hypothetical
2	69.5	13.8	744	2	S65669		biotin
3	68.5	13.6	1617	2	T28153		complement
4	67	13.3	283	2	AB3364		
5	67	13.3	538	2	T49849		related to

6	66	13.1	637	2	E70887	probable
fadD32 pr						
7	64.5	12.8	139	2	S70010	
glutamate/proline-						
8	64.5	12.8	415	2	T36965	hypothetical
prote						
9	63.5	12.6	493	1	S71634	stearoyl-CoA
9-des						
10	63	12.5	239	2	T08795	hypothetical
prote						
11	63	12.5	513	2	T48788	hypothetical
prote						
12	63	12.5	712	2	A47718	reverse
transcript						
13	62.5	12.4	861	2	I39714	cellulose
synthase						
14	62.5	12.4	1021	2	T10748	mannan endo-
1,4-be						
15	62	12.3	888	2	JC5399	dual leucine
zippe						
16	62	12.3	888	2	A55318	
serine/threonine p						
17	61.5	12.2	271	2	AB2095	hypothetical
prote						
18	61.5	12.2	567	2	F87594	conserved
hypothet						
19	61.5	12.2	632	2	S38042	probable
purine nu						
20	61.5	12.2	1343	2	T20718	hypothetical
prote						
21	61	12.1	117	2	A37178	neuromedin B
precu						
22	61	12.1	1002	2	AF2383	hypothetical
prote						
23	61	12.1	1263	2	T13805	spalt-
related prot						
24	61	12.1	1940	2	F75393	hypothetical
prote						
25	60.5	12.0	221	2	S70009	
glutamate/proline-						
26	60.5	12.0	352	2	T13600	hypothetical
prote						
27	60.5	12.0	425	2	C86232	hypothetical
prote						
28	60.5	12.0	623	2	T39001	probable
exonuclea						
29	60.5	12.0	946	2	S27921	nuclear
antigen EB						
30	60.5	12.0	1075	2	B96508	hypothetical
prote						
31	60.5	12.0	3839	2	T49799	related to
TOM1 pr						
32	60	11.9	147	2	A24580	gastrula-
specific						
33	60	11.9	227	2	T37134	hypothetical
prote						

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OM protein - protein search, using sw model

Run on: October 26, 2005, 04:34:00 ; Search time 25 Seconds  
(without alignments)  
268.737 Million cell

updates/sec

Title: US-10-644-807-213  
Perfect score: 505  
Sequence: 1 MDRRRMALRPGSRRPTAFF.....RWKPVAPRRMKACPQVLEW 90

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being  
printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
-----						
1	76.5	15.1	414	4	US-09-252-991A-27895	Sequence
27895, A						
2	76	15.0	335	4	US-09-252-991A-27013	Sequence
27013, A						
3	75	14.9	470	4	US-09-252-991A-27804	Sequence
27804, A						
4	74.5	14.8	283	4	US-09-270-767-41831	Sequence
41831, A						

5	74.5	14.8	428	4	US-09-252-991A-24452	Sequence
24452, A						
6	73	14.5	329	4	US-09-252-991A-19752	Sequence
19752, A						
7	71.5	14.2	578	4	US-09-252-991A-18656	Sequence
18656, A						
8	70.5	14.0	340	4	US-09-489-039A-7925	Sequence
7925, Ap						
9	70	13.9	117	4	US-09-252-991A-25484	Sequence
25484, A						
10	70	13.9	411	4	US-09-252-991A-28696	Sequence
28696, A						
11	69.5	13.8	155	4	US-09-252-991A-17230	Sequence
17230, A						
12	69.5	13.8	240	4	US-09-252-991A-17701	Sequence
17701, A						
13	69.5	13.8	412	4	US-09-252-991A-22952	Sequence
22952, A						
14	69.5	13.8	447	4	US-09-252-991A-27262	Sequence
27262, A						
15	69	13.7	175	4	US-09-252-991A-28806	Sequence
28806, A						
16	69	13.7	595	4	US-09-252-991A-30780	Sequence
30780, A						
17	68	13.5	622	4	US-09-252-991A-32308	Sequence
32308, A						
18	67.5	13.4	479	4	US-09-252-991A-32994	Sequence
32994, A						
19	67.5	13.4	500	4	US-09-848-726-2	Sequence 2,
Appli						
20	67.5	13.4	519	4	US-09-252-991A-28349	Sequence
28349, A						
21	67	13.3	171	4	US-09-252-991A-27874	Sequence
27874, A						
22	67	13.3	337	4	US-09-252-991A-17436	Sequence
17436, A						
23	67	13.3	564	4	US-09-252-991A-27329	Sequence
27329, A						
24	66.5	13.2	699	4	US-09-252-991A-17780	Sequence
17780, A						
25	66.5	13.2	959	4	US-09-252-991A-21747	Sequence
21747, A						
26	66	13.1	134	4	US-09-252-991A-18314	Sequence
18314, A						
27	66	13.1	469	4	US-09-252-991A-32604	Sequence
32604, A						
28	66	13.1	660	3	US-09-273-163-6	Sequence 6,
Appli						
29	65.5	13.0	242	4	US-09-252-991A-19038	Sequence
19038, A						
30	65.5	13.0	298	4	US-09-252-991A-20510	Sequence
20510, A						
31	65.5	13.0	312	4	US-09-252-991A-26762	Sequence
26762, A						
32	65.5	13.0	317	4	US-09-252-991A-31751	Sequence
31751, A						

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OM protein - protein search, using sw model

Run on: October 26, 2005, 04:33:09 ; Search time 59 Seconds  
(without alignments)  
781.138 Million cell

updates/sec

Title: US-10-644-807-213

Perfect score: 505

Sequence: 1 MDRRRMALRPGSRRPTAFF.....RWKPVAPRRMKACPQVLLEW 90

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being  
printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result			%				
No.	Score	Match	Query Length	DB	ID	Description	
-----							
1	76	15.0	361	2	Q7V7F1	Q7v7f1	
prochloroco							
2	75	14.9	241	2	Q84SK1	Q84sk1 oryza	
sativ							
3	75	14.9	279	2	Q8TVP8	Q8tvp8	
methanopyru							
4	75	14.9	615	2	Q6JWT6	Q6jwt6	
uncultured							
5	74	14.7	347	2	Q8CEP3	Q8cep3 mus	
musculu							
6	73.5	14.6	293	2	Q72JK8	Q72jk8	
thermus the							

7	73	14.5	323	2	Q7NDH7	Q7ndh7
gloeobacter						
8	73	14.5	615	2	Q62I62	Q62i62
burkholderi						
9	73	14.5	615	2	Q63RF7	Q63rf7
burkholderi						
10	72.5	14.4	425	2	Q64AJ0	Q64aj0
uncultured						
11	72.5	14.4	430	2	Q73Y36	Q73y36
mycobacteri						
12	72.5	14.4	500	2	Q8FMC7	Q8fmc7
corynebacte						
13	71.5	14.2	179	2	Q9UKB0	Q9ukb0 homo
sapien						
14	71	14.1	271	1	TRMB_STRCO	Q9f305
streptomyce						
15	71	14.1	426	2	Q64HX5	Q64hx5
oncorhynchu						
16	70.5	14.0	748	2	Q8XSE4	Q8xse4
ralstonia s						
17	70	13.9	379	2	Q9XF27	Q9xf27 oryza
sativ						
18	70	13.9	419	2	Q6XN82	Q6xn82
rhodococcus						
19	70	13.9	505	2	Q90Y96	Q90y96
cyprinus ca						
20	70	13.9	815	2	Q7S1R8	Q7slr8
neurospora						
21	70	13.9	995	2	Q9P3I0	Q9p3i0
neurospora						
22	69.5	13.8	744	1	BISC_RHOSH	P54934
rhodobacter						
23	69	13.7	218	2	Q6K7L9	Q6k7l9 oryza
sativ						
24	69	13.7	219	2	Q6Z7G4	Q6z7g4 oryza
sativ						
25	69	13.7	401	2	Q8N770	Q8n770 homo
sapien						
26	69	13.7	632	2	Q745L0	Q745l0
mycobacteri						
27	69	13.7	2754	2	Q7PRV4	Q7prv4
anopheles g						
28	68	13.5	177	2	Q6V0T7	Q6v0t7
uncultured						
29	68	13.5	391	2	Q6UQ62	Q6uq62
thermus sp.						
30	68	13.5	519	2	Q6C3N9	Q6c3n9
yarrowia li						
31	68	13.5	739	2	Q9LWY3	Q9lwy3 oryza
sativ						
32	68	13.5	928	2	Q92KH3	Q92kh3
rhizobium m						
33	68	13.5	2033	2	Q6UDF2	Q6udf2
psittacid h						
34	68	13.5	3649	2	Q83WE8	Q83we8
micromonosp						



GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: October 26, 2005, 04:34:40 ; Search time 172 Seconds  
(without alignments)  
218.465 Million cell

updates/sec

Title: US-10-644-807-213  
Perfect score: 505  
Sequence: 1 MDRRRMALRPGSRRPTAFF.....RWKPVAPRRMKACPQVLEW 90

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1862994 seqs, 417510619 residues

Total number of hits satisfying chosen parameters: 1862994

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep:\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*
- 21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	88	17.4	127	16	US-10-425-115-350087	Sequence
350087,						
2	85.5	16.9	141	18	US-10-450-763-49962	Sequence
49962, A						
3	80	15.8	142	16	US-10-437-963-175511	Sequence
175511,						
4	77.5	15.3	132	16	US-10-425-115-350089	Sequence
350089,						
5	77	15.2	375	15	US-10-425-114-72486	Sequence
72486, A						
6	76	15.0	202	9	US-09-925-299-974	Sequence
974, App						
7	76	15.0	202	10	US-09-925-299-974	Sequence
974, App						
8	75.5	15.0	211	16	US-10-388-838-110	Sequence
110, App						
9	75.5	15.0	211	16	US-10-388-838-114	Sequence
114, App						
10	75.5	15.0	211	17	US-10-741-600-1131	Sequence
1131, Ap						
11	75.5	15.0	211	17	US-10-741-600-1132	Sequence
1132, Ap						
12	75	14.9	303	16	US-10-437-963-181469	Sequence
181469,						
13	74	14.7	161	16	US-10-767-701-39394	Sequence
39394, A						
14	73.5	14.6	85	15	US-10-424-599-245104	Sequence
245104,						
15	73.5	14.6	194	16	US-10-425-115-192474	Sequence
192474,						
16	73	14.5	525	18	US-10-450-763-46425	Sequence
46425, A						
17	72.5	14.4	1981	16	US-10-437-963-195710	Sequence
195710,						
18	71.5	14.2	182	16	US-10-425-115-201930	Sequence
201930,						
19	71.5	14.2	329	15	US-10-425-114-50064	Sequence
50064, A						
20	71	14.1	263	16	US-10-425-115-241336	Sequence
241336,						
21	70.5	14.0	69	16	US-10-437-963-143865	Sequence
143865,						
22	70.5	14.0	603	15	US-10-329-027-3	Sequence
3, Appli						
23	70.5	14.0	760	15	US-10-074-978A-108	Sequence
108, App						
24	70	13.9	209	16	US-10-437-963-123523	Sequence
123523,						
25	70	13.9	215	16	US-10-437-963-191184	Sequence
191184,						